

M	R	R	K	E	K	R	L	Q	A	V	A	L	V	15	
CGGGGCTGACCCGGCCCCG	ATG	AGG	CGG	AAG	GAG	AAG	CGG	CTC	CTG	CAG	GCG	GTG	GCG	CTG	GTG
L	A	A	L	V	L	P	N	V	G	L	W	A	L	Y	R
CTG	GCG	GCC	CTG	GTC	CTC	CTG	CCC	AAC	GTG	GGG	CTT	TGG	GCG	CTG	TAC
P	D	G	T	P	G	G	S	G	A	A	V	A	P	A	G
CCC	GAC	GGC	ACC	CCT	GGG	GGG	GCA	TCG	GGG	GCG	GCG	GTG	GCG	CCG	GCG
H	S	R	Q	K	K	T	F	F	L	G	D	G	Q	K	L
CAC	AGT	CGA	CAA	AAG	AAA	ACG	TTT	TTC	TTG	GGA	GAT	GGG	CAG	AAG	CTG
D	K	E	A	I	R	R	D	A	Q	R	V	G	N	G	E
GAC	AAG	GAG	GCC	ATC	CGG	AGG	GAC	GCT	CAG	CGC	GTA	GGA	AAT	GGA	CAA
Y	P	M	T	D	A	E	R	V	D	Q	A	Y	R	E	N
TAC	CCC	ATG	ACC	GAT	GCT	GAG	AGA	GTG	GAT	CAG	GCA	TAC	CGA	GAA	AAT
Y	V	S	D	K	I	S	L	N	R	S	L	P	D	I	R
TAC	GTC	AGT	GAT	AAA	ATC	TCC	TTG	AAT	CGC	TCT	CCA	GAT	ATC	CGG	CAC
N	S	K	R	Y	L	E	T	L	P	N	T	S	I	I	I
AAC	AGC	AAG	CGC	TAC	CTG	GAG	ACA	CTT	CCC	AAC	ACA	AGC	ATC	CCC	TTC

Fig. 1A

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E	G	W	S	S	L	L	R	T	V	H	S	V	L	N	R	S	P	P	P	E	175
GAG	GGC	TGG	TCC	CTC	CTC	CGC	ACC	GTC	CAC	AGT	GTG	CTC	AAT	CGC	TCG	CCT	CCA	GAG	GAG	525	
L	V	A	E	I	V	L	V	D	D	F	S	D	R	E	H	L	K	K	P	195	
CTG	GTC	GCC	GAG	ATT	GTA	CTG	GTC	GAC	GAC	TTC	AGT	GAT	CGA	GAG	CAC	CTG	AAG	AAG	CCT	585	
L	E	D	Y	M	A	L	F	P	S	V	R	I	L	R	T	K	R	R	E	215	
CTT	GAA	GAC	TAC	ATG	GCC	CTT	TTC	CCC	AGT	GTG	AGG	ATT	CTT	CGA	ACC	AAG	AAA	CGG	GAA	645	
G	L	I	R	T	R	M	L	G	A	S	V	A	T	G	D	V	I	T	F	235	
GGG	CTG	ATA	AGG	ACC	CGA	ATG	CTG	GGG	GCC	TCA	GTG	GCA	ACT	GGG	GAT	GTC	ATC	ACA	TTC	705	
L	D	S	H	C	E	A	N	V	N	W	L	P	P	L	L	D	R	I	A	255	
TTG	GAT	TCA	CAC	TGT	GAA	GCC	AAT	GTC	AAC	TGG	CTT	CCC	CCC	TGG	CTT	GAC	CGC	ATT	GCT	765	
R	N	R	K	T	I	V	C	P	M	I	D	V	I	D	H	D	D	F	R	275	
CGG	AAC	CGC	AAG	ACC	ATT	GTG	TGC	CCG	ATG	ATT	GAT	GTA	ATT	GAC	CAT	GAC	GAC	TTT	CGG	825	
Y	E	T	Q	A	G	D	A	M	R	G	A	F	D	W	E	M	Y	Y	K	295	
TAC	GAG	ACA	CAG	GCA	GGG	GAT	GCC	ATG	CGG	GGA	GCC	TTT	GAC	TGG	GAG	ATG	TAC	TAC	AAG	885	
R	I	P	I	P	P	E	L	Q	K	A	D	P	S	D	P	F	E	S	P	315	
CGG	ATC	CCG	ATC	CCT	CCA	GAA	CTG	CAG	AAA	GCT	GAC	CCC	AGC	GAC	CCA	TTT	GAG	TCT	CCC	945	
V	M	A	G	G	L	F	A	V	D	R	K	W	F	W	E	L	G	G	Y	335	
GTG	ATG	GCC	GGT	GGA	CTG	TTC	GCC	GTG	GAT	CGG	AAG	TGG	TTC	TGG	GAA	CTC	GGC	GGG	TAT	1005	

Fig. 1B

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D	P	G	L	E	I	W	G	G	E	Q	Y	E	I	S	F	K	V	W	M	355
GAC	CCA	GGC	TTG	GAG	ATC	TGG	GGA	GGG	GAG	CAG	TAT	GAA	ATC	TCC	TTC	AAG	GTG	TGG	ATG	1065
C	G	G	R	M	E	D	I	P	C	S	R	V	G	H	I	Y	R	K	Y	375
TGT	GGG	GGC	CGC	ATG	GAG	GAC	ATC	CCC	TGC	TCC	AGG	GTG	GGC	CAT	ATC	TAC	AGG	AAG	TAT	1125
V	P	Y	K	V	P	A	G	V	S	L	A	R	N	L	K	R	V	A	E	395
GTG	CCC	TAC	AAG	GTC	CCG	GCC	GGA	GTC	AGC	CTG	GCC	CGG	AAC	CTT	AAG	CGG	GTG	GCC	GAA	1185
V	W	M	D	E	Y	A	E	Y	I	Y	Q	R	R	P	E	Y	R	H	L	415
GTG	TGG	ATG	GAT	GAG	TAC	GCA	GAG	TAC	ATT	TAC	CAG	CGC	CGG	CCT	GAA	TAC	CGC	CAC	CTC	1245
S	A	G	D	V	A	V	Q	K	K	L	R	S	S	L	N	C	K	S	F	435
TCC	GCT	GGG	GAT	GTC	GCA	GTC	CAG	AAA	AAG	CTC	CGC	AGC	TCC	C TT	AAC	TGC	AAG	AGT	TTC	1305
K	W	F	M	T	K	I	A	W	D	L	P	K	F	Y	P	P	V	E	P	455
AAG	TGG	TTT	ATG	ACG	AAG	ATA	GCC	TGG	GAC	CTG	CCC	AAA	TTC	TAC	CCA	CCC	GTG	GAG	CCC	1365
P	A	A	A	W	G	E	I	R	N	V	G	T	G	L	C	A	D	T	K	475
CCG	GCT	GCA	GCT	TGG	GGG	GAG	ATC	CGA	AAT	GTG	GGC	ACA	GGG	CTG	TGT	GCA	GAC	ACA	AAG	1425
H	G	A	L	G	S	P	L	R	L	E	G	C	V	R	G	R	G	E	A	495
CAC	GGG	GCC	TTG	GGC	TCC	CCA	CTA	AGG	CTA	GAG	GGC	TGC	GTC	CGA	GGC	CGT	GGG	GAG	GCT	1485
A	W	N	N	M	Q	V	F	T	F	T	W	R	E	D	I	R	P	G	D	515
GCC	TGG	AAC	AAC	ATG	CAG	GTA	TTC	ACC	TGG	AGA	GAG	GAC	ATC	CGG	CCT	GGA	GAC	GAC	GAC	1545

Fig. 1C

P	Q	H	T	K	F	C	F	D	A	I	S	H	T	S	P	V	T	L	535	
CCC	CAG	CAC	ACC	AAG	AAG	TTC	TGC	TTT	GAT	GCC	ATT	TCC	CAC	ACC	AGC	CCT	GTC	ACG	CTG	1605

Y	D	C	H	S	M	K	G	N	Q	L	W	K	Y	R	K	D	K	T	L	555
TAC	GAC	TGC	CAC	AGC	ATG	AAG	GGC	AAC	CAG	CTG	TGG	AAA	TAC	CGC	AAA	GAC	AAG	ACC	CTG	1665

Y	H	P	V	S	G	S	C	M	D	C	S	E	S	D	H	R	I	F	M	575
TAC	CAC	CCT	GTC	AGT	GGC	AGC	TGC	ATG	GAC	TGC	AGT	GAA	AGT	GAC	CAT	AGG	ATC	TTC	ATG	1725
N	T	C	N	P	S	S	L	T	Q	Q	W	L	F	E	H	T	N	S	T	595
AAC	ACC	TGC	AAC	CCA	TCC	TCT	CTC	ACC	CAG	CAG	TGG	CTG	TTT	GAA	CAC	ACC	AAC	TCA	ACA	1785
V	L	E	K	F	N	R	N	*												603
GTC	TTG	GAA	AAA	TTC	AAT	AGG	AAC	TGA												1812

GCCCTCATGCCCTTGGCAGCCCCCAGGGTCTGGCACTCACTGCAGACTTCCCTCTAAGGGAGGCAGGGCCCT  
 GTGGGCACIAGGTGTAAGGTGCTGGCCAAATGGTCAAGGGCTCTGATTCAAGGGCTGGGTCTGCCT  
 GGTCCCTGAGCCCCCTGAGTTGTGGGGTAGGGTGAAGAGCATATCCCACAAAGAGCCCCACAGGGAGCAGAACACTGCTT  
 TAATCCCTGCTGACATCACGGAAACAGGGAAACAGGGAAACAGGGCTTCAACTATGTCACATGTTGAACATTATGTTGGAG  
 AACACCAAGGTAGCCCTAGGCCACCCAAAGTGAAGTCCCTGGGAGCTTTAGTATGCCACTCATCTGCAGCAGCTCTGTC  
 TGCTTTAGAAACAAAGTAAATTCGCTGTTGGGGAAACATTGCAGTTACAGCTTGACAGCTTCTGTTCTGTC  
 AGAGTCCCTTGGGCTTTAGTTCTGCCGTCCCTGGGGAAACATTGCAGTTACAGCTTGACAGCTTCTGTTCTGTC  
 ACACCCAGGTGATTGGTCCGGTAAAGGCCATACTTGGGGCTAAGAGTGTCAAGTATTGAATGCTGATCAGCTG  
 CCAGGTGAGGAGTCAGAAGGGAGCCCCCTAGACATTCTGAGCTATGGACATGCCAGCAGCCAGCAAGGACACCAAGG  
 TCTGGGTATTGAAATGTCATTAGCAATTAGCAATTGTCATTGTCATTGTCATTGTCATTGTCATTGTCATTGTCATTGTC

**Fig. 1D**

AGATGGCCCTGAGCCCCACGGAAAGGCCAGGTAGACCTCCAAACTAGAAATGCTGGCTGATTGCCCTGATCCATGCTT  
CCATTCCCTGTCTCTCCCCAGGCAATTACTGGCCTGGCAAAGTGCCTCTGACCTCATCATGGTTCTAGTTCATACAGAA  
GAGTCTGGGGCTCCAGGATCAACTGTGGCAAAGTGCCTCTGACCTCATCATGGTTCTAGTTCATACAGAA  
CTCCAGAAATTAAAGAACTCTATAATTGGATTGCAAAACTAGGTGCTACATAGGATCTGGTATTCCACATCCAAATA  
TGGATTCTAGAATGCTGTGATTAAGGAGCCAGCCAGGTGTAATAACAGTCAGGAGCCCCAGCCTAGAGACAATCT  
GTGAAATCCAAAAGTGGTGGGGACATGTGTCAGCTCAGCAGGGCTCAGCAGGGCTCAGGAGGGACATGTGTCAG  
GTCCTGGTGAAGAACCTGCACCCCTGGAACCTCCCACCATCATCACAAACTGTAGTCTCATTTGCAGTGAGAAAGAAC  
CCGACGTCCACAGCCAGATATAACCCAGCTCCATGCCAGCCCTCATGTTACCTTTGCTTATTACATGTC  
AGACTCCTAGGGCCTCCAGACTATAGGAAGCATTCTGTAACCAACCTGCCACCACAGATTGAAATGGAATC  
ACATTCCACAAATCTATGGCTTCCACAGCTAGCCAGAAATAACTTGAATCAGCATCCAAATTAGTAGTTGAGTCTCTT  
GATTGTGTCAATTACCAATTAAATAACTGAGACCTAAGTCTGGAAACAGAGGCCACGAAATCTGCCTTGAGATGCTGGCA  
GATCTCAAGGCCATCAATTATTGGGGAGGGACAAACACTCCCAATCACCAGTCAAGTGGCTGAGCTGAAATGTTAGCT  
GGCGAGGAATTACTCCACTTCTGGCCAGCACAAAGCCCTGCTTGGCCACCTGTGCTGCAAGAGGGCCCCCTGTGC  
TTGCAACGGCTTACGTGTTGATCCAGTGTCCATTCAATGAGTGTAGCTTAGAAGTGGCCCTATAGAAAGA  
AGTCAAAAGATGAGGGCCCTCTAGAATCTAGGATAACAAGAGTGTGACAGTTGAGGAGTCAATTGAGATTCATCA  
TCAAAGAGCAATGCCAGCGTICGTAAAAATAACTGTCGCTTAAAGAAAATGCAAATAGCAAAATCCCTAA  
ACTTGAAAAAA

Fig. 1E

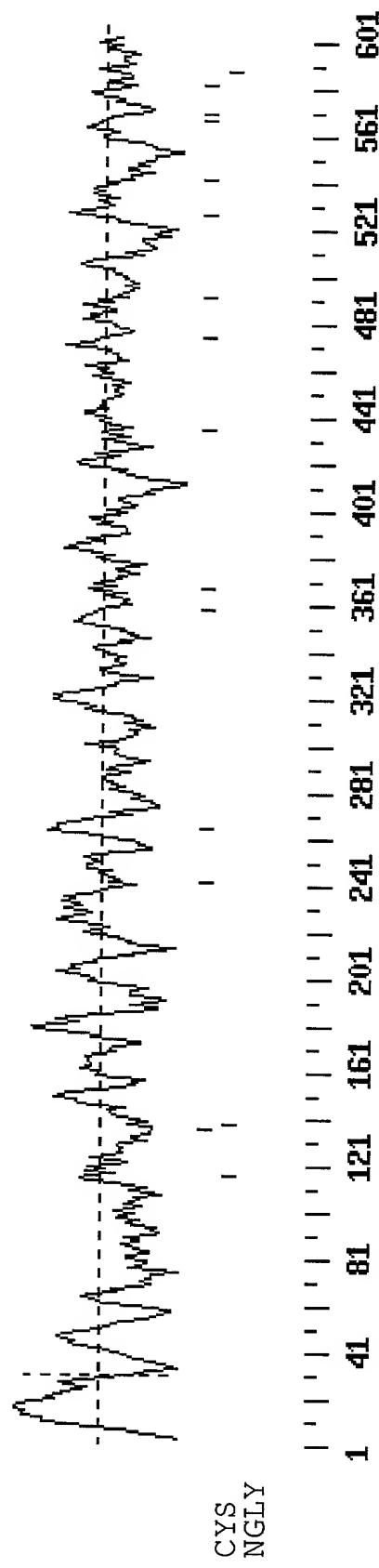


Fig. 2

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M	A	A	G	E	R	S	W	C	L	C	K	L	R	F	F	17			
TCGGGGAAAG	ATG	GCG	GCC	GGC	GAA	AGG	AGC	TGG	TGC	CTG	TGC	AAG	TTG	AGG	TTT	51			
Y	S	L	F	F	P	G	L	I	V	C	G	T	L	C	V	137			
TAT	TCA	TTA	TTC	TTC	CCT	GGG	CTC	ATT	GTA	TGT	GGA	ACT	TTA	TGT	GTG	TTG	ATT	111	
V	L	W	G	I	R	L	L	Q	R	K	K	L	V	S	T	S	K	57	
GTC	CTT	TGG	GGA	ATC	AGA	CTG	CTG	CTA	CAG	AGA	AAG	AAA	TTA	GTG	TCA	ACT	AGC	AAA	171
N	G	K	N	Q	M	V	I	A	F	F	H	P	Y	C	N	A	G	G	77
AAT	GGG	AAA	AAT	CAA	ATG	GTG	ATT	GCA	TTT	TTT	CAT	CCA	TAC	TGC	AAT	GCT	GGT	GGA	231
G	E	R	V	L	W	C	A	L	R	A	L	Q	K	K	Y	P	E	A	97
GAA	GAA	AGA	GTT	TTA	TGG	TGT	GCT	TTA	AGA	GCC	CTG	CAG	AAA	AAG	TAT	CCT	GAA	GCA	291
Y	V	V	Y	T	G	D	V	N	V	N	G	Q	Q	I	L	E	G	A	117
TAT	GTT	GTT	TAT	ACC	GGC	GAT	GTT	AAT	GTC	AAC	GGT	CAA	CAG	ATA	CTA	GAA	GGT	GCT	351
R	R	F	N	I	R	L	I	H	P	V	Q	F	V	F	L	R	K	R	137
AGA	AGA	TTT	AAC	ATC	AGA	TTA	ATT	CAC	CCA	GTG	CAG	TTT	GTT	TTT	TTA	AGG	AAA	CCG	411
L	V	E	D	S	L	Y	P	H	F	T	L	L	G	Q	S	L	G	S	157
CTT	GTG	GAA	GAT	TCA	CTG	TAT	CCT	CAC	TTC	ACA	CTG	GGC	CAA	AGT	CTA	GGA	TCC	ATT	471
F	L	G	W	E	A	L	M	Q	C	V	P	D	V	Y	I	D	S	M	177
TTT	CTT	GGC	TGG	GAA	GCT	CTA	ATG	CAG	TGT	TTT	CCT	GAT	GTT	TAC	ATT	GAT	TCA	ATG	531

**Fig. 3A**

Y	A	F	T	L	P	L	F	K	Y	I	G	G	C	Q	V	G	S	Y	V	197
TAC	GCT	TTT	ACG	CTT	CCT	CTG	TTT	AAG	TAT	ATA	GGG	GGT	TGC	CAA	GTT	GGA	AGC	TAT	GTT	591
H	Y	P	T	I	S	T	D	M	L	S	V	V	K	N	Q	N	I	G	F	217
CAT	TAT	CCT	ACT	ATC	AGC	ACC	GAC	ATG	CTC	TCT	GTA	GTG	AAG	AAT	CAA	AAT	ATT	GGA	TTT	651
N	N	A	A	F	I	T	R	N	P	F	L	S	K	V	K	L	I	Y	Y	237
AAT	AAT	GCA	GCC	TTC	ATT	ACC	AGG	AAT	CCT	TTT	CTC	AGC	AAA	GTA	AAG	CTC	ATC	TAC	TAC	711
Y	L	F	A	F	I	Y	G	L	V	G	S	C	S	D	V	V	M	V	N	257
TAT	TTA	TTT	GCT	TTT	ATT	TAT	GGT	CTT	GTT	GGT	TCT	TGC	AGT	GAT	GTA	GTC	ATG	GTC	AAT	771
S	S	W	T	L	N	H	I	L	S	L	W	K	V	G	N	C	T	N	I	277
TCT	TCT	TGG	ACA	CTA	AAC	CAT	ATT	CTC	TCA	CTA	TGG	AAA	GTT	GGG	AAT	TGC	ACT	AAC	ATT	831
V	Y	P	P	C	D	V	Q	T	F	L	D	I	P	L	H	E	K	K	M	297
GTT	TAT	CCA	CCT	TGT	GAT	GTG	CAG	ACA	TTT	CTG	GAC	ATT	CCC	TTA	CAT	GAG	AAA	AAG	ATG	891
T	P	G	H	L	L	V	S	V	G	Q	F	R	P	E	K	N	H	P	L	317
ACC	CCA	GGA	CAT	TTG	CTG	GTT	TCT	GTT	GGC	CAG	TTT	AGG	CCG	GAA	AAG	AAT	CAT	CCA	TTG	951
Q	I	R	A	F	A	K	L	L	N	K	K	M	V	E	S	P	P	S	L	337
CAG	ATC	AGA	GCC	TTT	GCT	AAA	TTG	CTG	AAT	AAG	AAT	AGG	ATG	GTT	GAG	TCA	CCT	CTG	CTT	1011
K	L	V	L	I	G	G	C	R	N	K	D	D	E	L	R	V	N	Q	L	357
AAA	CTT	GTC	CTC	ATT	GGA	GGT	TGT	CGT	AAC	AAA	GAT	GAA	CTT	AGG	GTA	AAC	CAA	CTG	1071	

**Fig. 3B**

R	R	L	S	E	D	L	G	V	Q	E	Y	V	E	F	K	I	N	I	P	377
AGA	AGG	CTG	TCT	GAG	GAT	TTA	GGA	GTT	CAA	GAA	TAT	GTG	GAA	TTT	AAA	ATA	AAC	ATT	CCA	1131
F	D	E	L	K	N	Y	L	S	E	A	T	I	G	L	H	T	M	W	N	397
TTT	GAT	GAA	TTA	AAG	AAT	TAT	TTG	TCT	GAA	GCA	ACA	ATT	GGT	CTG	CAT	ACC	ATG	TGG	AAC	1191
E	H	F	G	I	G	V	V	E	C	M	A	A	G	T	I	I	L	A	H	417
GAG	CAT	TTT	GGG	ATT	GGA	GTT	GTG	GAG	TGT	ATG	GCA	GCT	GGC	ACA	ATT	ATC	CTT	GCA	CAC	1251
N	S	G	G	P	K	L	D	I	V	V	P	H	E	G	D	I	T	G	F	437
AAT	TCG	GGG	GGC	CCA	AAG	CTT	GAC	ATT	GTG	GTT	CCT	CAC	GAA	GGA	GAT	ATA	ACT	GGC	TTT	1311
L	A	E	S	E	E	D	Y	A	E	T	I	A	H	I	L	S	M	S	A	457
CTG	GCT	GAG	AGT	GAA	GAA	GAC	TAT	GCT	GAA	ACT	ATC	GCT	CAC	ATT	CTT	TCC	ATG	TCT	GCA	1371
E	K	R	L	Q	I	R	K	S	A	R	A	S	V	S	R	F	S	D	Q	477
GAA	AAG	AGA	CTC	CAA	ATC	AGA	AAA	AGT	GCT	CGT	GCA	TCT	GTA	AGC	AGA	TTC	TCT	GAT	CAG	1431
E	F	E	V	T	F	L	S	S	V	E	K	L	F	K	*					492
GAA	TTT	GAA	GTG	ACA	TTC	CTA	TCA	TCT	GTG	GAA	AAG	TTA	TTT	AAG	TAA					1479

TGCCATATCTGTAAATTAAAGATATTATATAAACTGGTAAACACCTCATATGTAATATTCTAAATTCAAT  
 CTCAATTGTCAAATCATTACTTAGAAAACAGACAAAATTCCCTTTAGAATAAAAGGAAGTGTGAAAGAAATG  
 GATGACTAGCCTTGGCTTCCATTCTGGTATACATGAGAGAGGCTGGCTGCTGAGATGAATGTGAACTGGG  
 GAAATTCTGGCTTGAGCCACAGGAAGAACTAGTGGATTGAGTGAATAACTACCCCTTGAGTGAAGATGAGGG

**Fig. 3C**

**Fig. 3D**

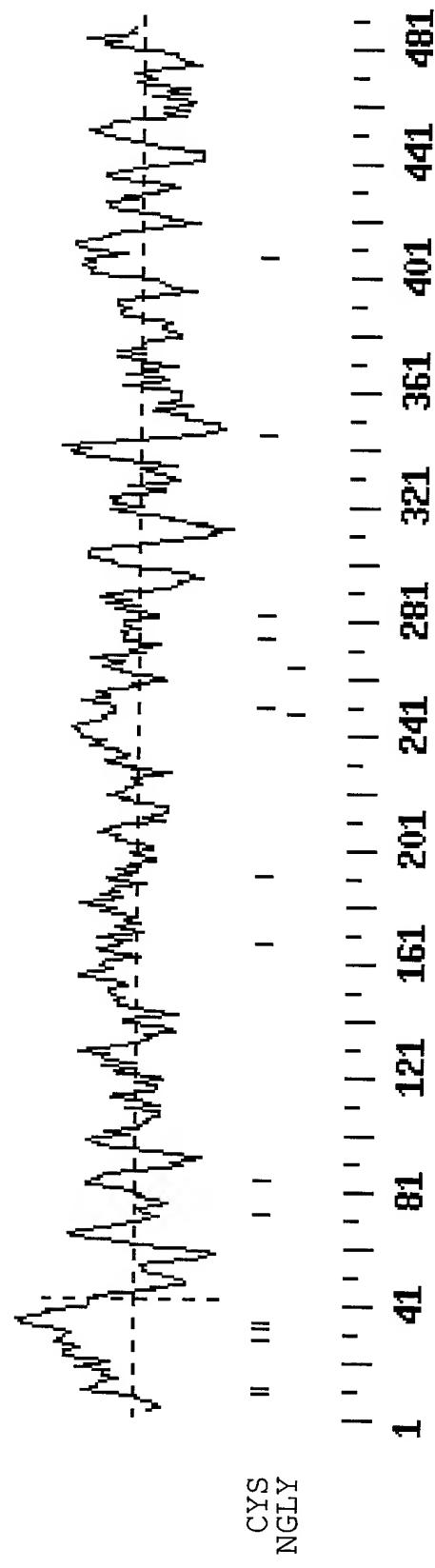


Fig. 4

MUS	GT1	MRKFAVCKVVVLATSL	VWVLLDMFLLLYESE	CNKCEEKQERGLPAG
RAT	GT1	MRKFAVCKVVVLATSL	VWVLLDMFLLLYESE	CNKCEEKKERGLPAG
HUM	GT1	MRKFAVCKVVVLATSL	IWVLLDMFLLLYESE	CNKCDEKKERGLPAG
COW	GT1	MRKFAVCKVVVLATSL	IWVLLDMFLLLYESE	CNKCDEKKERGLPAG
PIG	GT1	MRKFAVCKVVVLATSL	IWVLLDMFLLLYESE	CNKCDEKKERGLPAG
<b>47169</b>	<b>---MRRREKRRLIQQAV</b>	<b>ALVLAALVLLIPNVGL</b>	<b>WALYRERQPDGTPEGG</b>	<b>SGAAVAPAAGQGSHS</b>
MUS	GT1	-----	GEMGKPVVIPIKEDQE	KMKEMFKINQFNLM
RAT	GT1	-----	GEMGKPVVIPIKEDQE	KMKEMFKINQFNLM
HUM	GT1	-----	GEMGKPVVIPIKEDQE	KMKEMFKINQFNLM
COW	GT1	-----	GEMGKPVVIPIKEDQE	KMKEMFKINQFNLM
PIG	GT1	-----	GEMGKPVVIPIKEDQE	KMKEMFKINQFNLM
<b>47169</b>	<b>RQKTKFFFLGDGQKLK</b>	<b>DWDKEAIRDAQRV</b>	<b>GNGEQGRPYPMTDAE</b>	<b>RVDQAYRENGFNIYV</b>
MUS	GT1	SEMIALNRSLPPDVRL	EGCKTKVYPDNLPPT	SVVIVFHNEAWSTLL
RAT	GT1	SEMIAFNRSLPPDVRL	EGCKTKVYPDSLPTT	RTVHSVINRSPRHMI
HUM	GT1	SEMIALNRSLPPDVRL	EGCKTKVYPDNLPPT	RTVHSVINRSPRHMI
COW	GT1	SEMIALNRSLPPDVRL	EGCKTKVYPDNLPPT	RTVHSVINRSPRHMI
PIG	GT1	SEMIALNRSLPPDVRL	EGCKTKVYPDNLPPT	RTVHSVINRSPRHMI
<b>47169</b>	<b>SDKISLNRSLPPDIRH</b>	<b>PNCNSKRYLEELPN</b>	<b>SIIIFHNEGWSILL</b>	<b>RTVHSVINRSPPELV</b>

Fig. 5A

MUS_GT1	EEIVLVDDASERDFL	KRPLESYVKKLIKVVPV	HVIRMEQRSGLIRAR	LKGAAAVSRGQVITFL	
RAT_GT1	EEIVLVDDASERDFL	KRPLESYVKKLIKVVPV	HVIRMEQRSGLIRAR	LKGAAAVSKGQVITFL	
HUM_GT1	EEIVLVDDASERDFL	KRPLESYVKKLIKVVPV	HVIRMEQRSGLIRAR	LKGAAAVSKGQVITFL	
COW_GT1	EEIVLVDDASERDFL	KRPLESYVKKLIKVVPV	HVIRMEQRSGLIRAR	LKGAAAVSKGQVITFL	
PIG_GT1	EEIVLVDDASERDFL	KRPLESYVKKLIKVVPV	HVIRMEQRSGLIRAR	LKGAAAVSKGQVITFL	
<b>47169</b>	<b>AEIVLVDDFSDREHL</b>	<b>KKPLEDYMALEPS-V</b>	<b>RILRTKKREGLIRTR</b>	<b>MLGASVATGDVITFL</b>	
: :					
MUS_GT1	DAHCECTAGWILEPLL	ARIKHDRRTVVCPII	DVISDDTFEYMAGS-	DMTYGGGENWKLNFRW	
RAT_GT1	DAHCECTVGWILEPLL	ARIKHDRRTVVCPII	DVISDDTFEYMAGS-	DMTYGGGENWKLNFRW	
HUM_GT1	DAHCECTVGWILEPLL	ARIKHDRRTVVCPII	DVISDDTFEYMAGS-	DMTYGGGENWKLNFRW	
COW_GT1	DAHCECTVGWILEPLL	ARIKHDRRTVVCPII	DVISDDTFEYMAGS-	DMTYGGGENWKLNFRW	
PIG_GT1	DAHCECTVGWILEPLL	ARIKHDRRTVVCPII	DVISDDTFEYMAGS-	DMTYGGGENWKLNFRW	
<b>47169</b>	<b>DSHCEANVNWLPLL</b>	<b>DRIARNRKTIVCPMI</b>	<b>DVIDHDDFRTYETQAG</b>	<b>DAMRGAFDWEMYYKR</b>	
: :					
MUS_GT1	YPVPQREMDRRKGDR	TLPVRPTMAGGLFS	IDRDYEQEIGTYDAG	MDIWGGGENLEISFRI	
RAT_GT1	YPVPQREMDRRKGDR	TLPVRPTMAGGLFS	IDRDYEQEIGTYDAG	MDIWGGGENLEISFRI	
HUM_GT1	YPVPQREMDRRKGDR	TLPVRPTMAGGLFS	IDRDYEQEIGTYDAG	MDIWGGGENLEISFRI	
COW_GT1	YPVPQREMDRRKGDR	TLPVRPTMAGGLFS	IDRDYEQEIGTYDAG	MDIWGGGENLEISFRI	
PIG_GT1	YPVPQREMDRRKGDR	TLPVRPTMAGGLFS	IDRDYEQEIGTYDAG	MDIWGGGENLEISFRI	
<b>47169</b>	<b>IPIPP---ELQKADP</b>	<b>SDPFESPVMAGGLEA</b>	<b>VDRKWEWLGGYDPG</b>	<b>LEIWGGEQYEISFKV</b>	
: :					

Fig. 5B

MUS_GT1	WQCGGTLEIVTC SHV	GHVFRKATPYTFPGG	TGQIINKNNRRLAEV	WMDEFKNFFYIISPG
RAT_GT1	WQCGGTLEIVTC SHV	GHVFRKATPYTFPGG	TGQIINKNNRRLAEV	WMDEFKNFFYIISPG
HUM_GT1	WQCGGTLEIVTC SHV	GHVFRKATPYTFPGG	TGQIINKNNRRLAEV	WMDEFKNFFYIISPG
COW_GT1	WQCGGTLEIVTC SHV	GHVFRKATPYTFPGG	TGQIINKNNRRLAEV	WMDEFKNFFYIISPG
PIG_GT1	WQCGGTLEIVTC SHV	GHVFRKATPYTFPGG	TGQIINKNNRRLAEV	WMDEFKNFFYIISPG
<b>47169</b>	<b>WMCGGRMEDIPCSRV</b>	<b>GHIYRKXVPYKV P--</b>	<b>AGVSLARNLKRVAEV</b>	<b>WMDEAYEAYIYQRRE</b>
: : : : :	: : : : :	: : : : :	: : : : :	: : : : :
MUS_GT1	VTKV DYGDISSRLGL	RRKLQCKPESWYLEN	IYPDS-----	QIPRH
RAT_GT1	VTKV DYGDISSRVGL	RHKLQCKPESWYLEN	IYPDS-----	QIPRH
HUM_GT1	VTKV DYGDISSRVGL	RHKLQCKPESWYLEN	IYPDS-----	QIPRH
COW_GT1	VTKV DYGDISSRLGL	RHKLQCRPFSWYLEN	IYPDS-----	QIPRH
PIG_GT1	VTKV DYGDISSRLGL	RHKLQCRPFSWYLEN	IYPDS-----	QIPRH
<b>47169</b>	<b>YRHL SAGDVA VQKKL</b>	<b>RSSLNCKSEKWMETK</b>	<b>IAWDLFKEYPPVPEPP</b>	<b>AAAWGEIRNVGTGLC</b>
: : : : :	: : : : :	: : : : :	: : : : :	: : : : :
MUS_GT1	LDNMARKENEKV GIF	NCHGMGG-----	-NQ	VFSYTANKEIR-----
RAT_GT1	LDNMARKENEKV GIF	NCHGMGG-----	-NQ	VFSYTANKEIR-----
HUM_GT1	LDNMARKENEKV GIF	NCHGMGG-----	-NQ	VFSYTANKEIR-----
COW_GT1	LDNMARKENEKV GIF	NCHGMGG-----	-NQ	VFSYTANKEIR-----
PIG_GT1	LDNMARKENEKV GIF	NCHGMGG-----	-NQ	VFSYTANKEIR-----
<b>47169</b>	<b>ADTKH GALGSPLRLE</b>	<b>GCVR GRGEEA WNMQ</b>	<b>VETETTWREDIRPGDP</b>	<b>QHTKKFCFDATSHS</b>
: . . . :	: . . . :	: . . . :	: . . . :	: . . . :

Fig. 5C

MUS_GT1	PVTMLKCHHILKGQL	WEYDPVKLTLQHVNS	NQCLDKATEEDSQVP	SIRDCTGSRSSQQWLL
RAT_GT1	PVTMLKCHHILKGQL	WEYDPVKLTLQHVNS	NQCLDKATEEDSQVP	SIRDCTGSRSSQQWLL
HUM_GT1	PVTMLKCHHILKGQL	WEYDPVKLTLQHVNS	NQCLDKATEEDSQVP	SIRDCTGSRSSQQWLL
COW_GT1	PVTMLKCHHILKGQL	WEYDPVKLTLQHVNS	NQCLDKATEEDSQVP	SIRDCTGSRSSQQWLL
PIG_GT1	PVTMLKCHHILKGQL	WEYDPVKLTLQHVNS	NQCLDKATEEDSQVP	SIRDCTGSRSSQQWLL
<b>47169</b>	<b>PVTLYDCHSMRKGQL</b>	<b>WKYR-KDKTLIHPVS</b>	<b>GSCMDCS-ESDHRIF</b>	<b>MNTCMNPSSLIQQWLF</b>
MUS_GT1	R--NVTLPEIF---			
RAT_GT1	R--NVTLPEIF---			
HUM_GT1	R--NVTLPEIF---			
COW_GT1	R--NVTLPEIF---			
PIG_GT1	R--NVTLPEIF---			
<b>47169</b>	<b>EHTNSTVLEKENRN</b>			

Fig. 5D

g1y-5b ---M1IFKKKAI1K VILLVVPFWICSL1F FAATSNDSSQIGSNN DLANK--IAEANFHP  
g1y-6a --MIASLIRSRRRSR RCVVYSVFLFGFL1L WGSFALALVFLSDMY IGEDQ--ISTQKA1K  
g1y-3 --MLSVGGRSAVCR AVIATSIIVWLLIDVV ILFYYLDPSTSQQP FPEDNRILNRARRIE  
g1y-4 ----MLPRMLKMKT VGTVLAVIWLFGLAF IYVQSTSSSLRPPGR HPPPLP--QLDPLIP  
g1y-9 ----MLRYITIPRKK GTFVIAAFFLTVAEFC IVAYHRNDRRTKFQ FPDIEKYAAELVRLP  
**47169** -----MIRKEKERLL QAVALVIAALVLLPN **VGLWALLYERQPDG1T PGGSGAAVAPAAGQG**

g1y-5b KAAKQDV1QGFGPPI EPEPVENNKKVEEEE QPGGNLAKPKFMVDP NDPPIYKKGDAAQAGE  
g1y-6a PIARSNYHVVVGHYN GNLPEDKKNLTSEE LNAN-----LYAP HD-----DWGE  
g1y-3 PLPPAAQHDSDPDAH PIQPEKQEKOVYPVD KETANQLRKLMETQA FGPG-----YHGQ  
g1y-4 QNPPQNDEIRPKSA PPIPTINLAEDTTIH ERTEKD----VT---- -----WKT  
g1y-9 ETWNGEIHQ1PNTYA PR--EGP-----GE-----GE  
**47169** **SNSRQKRTFFLGDGQ** KLKDWHDKEARRDA QRVGN-----GE-----GE

g1y-5b LGKAVVVVDKTKLSTE EKAKYDKGMLNNAFN QYASDMISVHRTLPT NIDAECKT---EKYN  
g1y-6a GG--AGVS--H1TPE QQKLADSTFAVNQFN LLVSDG1SVRRSLPE IRKPSCRN---MTYP  
g1y-3 GGTGVTVP-----ED KKT1KEKRFLENQFN VVASEM1SVNRTL1PD YRSDACRTSGNNLKT  
g1y-4 FDVEKFLN-----KG KWHQGEDKYKANSFN QEASDALNPTRK1PD SREPOCRD--VDYSK  
g1y-9 KGKPVVVI1G-----K DAELGQADMKKWEMN VHASDK1SLDRDVPD PRIQACKD--IKYDY  
**47169** **QGRPYPM1-----DAERVDPAYRENGFN IYVSDK1S1NRS1L1PD IRHPNCNS---KRYL**

Fig. 6A

g1y-5b	ENLPRTSVIICFHNE	AWSVILLRTVHSVLER	TPDHILLEVVLVDDF	SDMDHTKRP-LEEVY
g1y-6a	DNLPTTSVIIVYHNE	AYSTILLRTVWSVDR	SPKEILIKEIIILVDDF	SDREELRYPILDTTL
g1y-3	AGMPKTSIIIVEHNE	AWTILLRTLHSVNR	SPRHILLEIIILVDDK	SDRDYLVKP-LDSYI
g1y-4	VGMQPTTVIITYHNE	ARSSILLRTVFSVENQ	SPEELILLEIIVLVDDN	SQDVEIGKE-L----
g1y-9	AALPKTSVIIIFTDE	AWTPILLRTVHSVNR	SPPEILLQEVILLDDN	SKRQELOQEP-LDEHT
<b>47169</b>	<b>ETLENITSITIPEHNE</b>	<b>GWSILLRTVHSVLRN</b>	<b>SPPELLVAEIVLVDDF</b>	<b>SDREELKRP-LEDY-</b>
g1y-5b	--SQFGGGKVKILRME	KREGGLIRARIIRGAAV	ATGEVVLTYLDOSHCEC	MEGWMEPLLDRIKRD
g1y-6a	--KPLPTDIKIIRSK	ERVGLLIRARMGQAQE	AQGDVLTFLDSHCEC	TKGWILEPLLTRIKLN
g1y-3	--KMFPPIPHLVHLE	NRSGLLIRARLITGSEM	AKGKILLFLDAHVEV	TDGWILEPLVSRRVAED
g1y-4	--AQIQORITVILRNN	QREGGLIRSRVKGAAQV	ARAPVLTFLDSHIEC	NQKWLIEPLLARIAEN
g1y-9	--KREFGGKVRLIRKH	DRHGLLIRAKLAGARE	AVGDIIVFLDSHCEA	NHGWLIEPIVQRISDE
<b>47169</b>	<b>--MALEPSVRILRTK</b>	<b>KREGGLIRTRMLGASV</b>	<b>ATGDVITFLDSHCEA</b>	<b>NVNWLIPPLIDRIARN</b>
g1y-5b	PTIVVCPVIDVIDDN	TFEYHHSKAYFETSV-	-GGFDWGLQENWHSI	P-ERDRKNRTRPIDI
g1y-6a	RKAIVPCPVIDIIINDN	TFQYQKGKGIEMFR---	-GGFNWNLQFRWYGM	PTAMAKQHLLDPTGP
g1y-3	RKRVVAPIIIDVISDD	TFEYVVTASETTWG--	--GFTNWHLNFRWYAV	PKRELLNRGSDRSMP
g1y-4	PKAVVAPIIIDVINVD	NFNYVGASADLR---	--GGFDWTLVERWEFM	NEQLRKERHAHPTAP
g1y-9	RTAIIVCPMIDSISDN	TLAYHGDWSLST---	--GGFSWALHETWEGL	S-EEEQKRRTKPTDY
<b>47169</b>	<b>RKTIVCPMIDVIDHD</b>	<b>DFTYETQAGDAMR</b>	<b>-GAFTDWEMYKRIP</b>	<b>P---PELQKADPSDP</b>

Fig. 6B

g1y-5b	VRSPTMAGGLFSIDK	EYEEKLGTYDPGFDI	WGGENLELSFKIWMC	GGTLEIVPCSHVGHV
g1y-6a	IESPTMAGGLESINR	NYFEELGEYDPGMDI	WGGENLEMSFRIWQC	GGRVEILPCSHVGHV
g1y-3	IQTPTIAGGLFAIDK	QFYDYGSYDEGMQV	WGGENLEISFRVWMC	GGSLEIHPCSRVGHV
g1y-4	IRSPTMAGGLFAISK	EWENELGTYDLDMEV	WGGENLEMSFRVWQC	GGSSLEIMPCSRVGHV
g1y-9	IRSPTMAGGLLAANR	EYFFEVGGYDEEMDI	WGGENLEISFRAWMC	GGSIEFIPCSHVGHF
<b>47169</b>	<b>FESPVMAGGLEAVDR</b>	<b>KWFWELEGGYDPLGEI</b>	<b>WGGEQYEISEKUWMC</b>	<b>GGRMEDIPCSRVGHTI</b>
g1y-5b	FRKRSPTYKWR---TG	VNVLKRN SIRLAEVW	LDDYKTYYYERIN--	NQLGDFGDISSRKKKL
g1y-6a	FRKS S SPHDFPGK-SS	GKV LNTNLLRVAEVW	MDDWKHYFYKIA PQA	HRMRSS IDV S ERVEL
g1y-3	FRK QTPYTFPG---GT	AKV IHHNAARTAEVW	MDE YK AFFYK MV P-A	ARNVEAGDV SERKKL
g1y-4	FRKKH PYTFPG---GS	GNV FOKNTRRAAEVW	MDE YKAI YLK NV P-S	ARFVN EFG DIT DRLAI
g1y-9	FRAGHPYNNMTGRNNN	KDV HGTNSKERLAEVW	MDDYKRLYYMHRED-	LRTKDVGDLTARH E L
<b>47169</b>	<b>YRKVVPYKVP---A</b>	<b>GVSLARNLKRVAEVW</b>	<b>MDEYYAEYIYQRRP-E</b>	<b>YRHL SAGDVA VQKKL</b>
g1y-5b	RE DLGCKSF KWYLDN	IYP-ELFVPGESVAK	GEVRNSAVQPARCLD	CMVGRHEKNRPV GFTY
g1y-6a	RKKLNCKSF KWYLN	VFQ-DHFLPTPLD RF	GRMTSSS-NSSVCLA	WTLRSSGIKTA STAD
g1y-3	RET LQCKSF KWYLEN	IYP-EAPLPADFRSL	GAIVN----RFTEKC	VDTNGKKDGQAPGQ
g1y-4	RDR LQCKSF KWYLEN	VYP-QLEIPRKTPGK	SFQMKIG----NLC	LD SMARKESEAPGLF
g1y-9	RKR LNCKPF KWFLDN	I A KGGKFIM DEDVVAY	GALHTVVSGTRMCTD	TLQRDEKMSQ LLGVF
<b>47169</b>	<b>RSSLNCKSF KWFMTR</b>	<b>I A WDLPKF YPPVEPP</b>	<b>AA AWGEI RNV GTGLC</b>	<b>ADTKHNGALGSPRLKE</b>

Fig. 6C

g1y-5b	QCHGQQGGN-----Q	YWMLSKDGEIRRDE-----	SCVDYAGS DVMVEPCHGMKGNNQE
g1y-6a	CLKIFHKT-----Q	LWLYTGDRRIRTDEH-----	WKIQIILKECAGFDTEY
g1y-3	ACHGAGGN-----Q	AWSLTGKGEIRSDDL-----	KLERCSVSKINVKHV
g1y-4	GCHGTGGN-----Q	EWVFDQLTKTFKNAI-----	SQLCIDESSN TENKTVTMVKCENLR
g1y-9	HCQGKGSSP-----Q	LMSLSKEGNLIRREN-----	TCASEEN GNIRMKTCSKAQFN
<b>47169</b>	<b>GCVRGRGEAAWNNMQ</b>	<b>VETFTIWREDIRPGDP</b>	<b>QHTKKFCEFDALISHTS PVTLLDCHSMKGNNQI</b>
.	.	.	.
g1y-5b	WRYNHDTGRLQHAVS	QKCLIG-----MTK	DGAKLEMVACQYDDP YQHWKFKEYNEAKAI
g1y-6a	WDFKPKIGRFQNRKT	EFCLASPDIFDPTKD	RQNWTITEMSWLPEH
g1y-3	FVFFDDQAGTLLHKKT	GKCVTG-----AD	-QMWQLEGYQSP---
g1y-4	PDTMVVEKNGWLTOG	QRVTILDDECGLGRKD-	AQRWIFEKLDDTYE--
g1y-9	ERWAYENKMIRNLKS	GDWLIIYGAHCELNNG	HQKWNFLIDPAKA---
<b>47169</b>	<b>WKYRKDK-TLYHPVS</b>	<b>GSCMDCS-----ES</b>	<b>DHRITEMNTCNPSSIT -QOWLFEHTNSTVLE</b>
.	.	.	.
g1y-5b	EHGAKPPS		
g1y-6a	P-----		
g1y-3	-----		
g1y-4	-----		
g1y-9	-----		
<b>47169</b>	<b>KFNERN---</b>		

Fig. 6D